



## **RAW SEQUENCE LISTING** **ERROR REPORT**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/782,974  
Source: OIP/E  
Date Processed by STIC: 3/27/2001

**THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.**

**PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:**

- 1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
- 2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

**FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.**

**FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.**

**PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)**

**PATENTIN 3.0 e-mail help: [patin3help@uspto.gov](mailto:patin3help@uspto.gov) or phone 703-306-4119 (R. Wax)**

**TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:**

### **Checker Version 3.0**

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

**Checker Version 3.0 can be down loaded from the USPTO website at the following address:**

**<http://www.uspto.gov/web/offices/pac/checker>**

# Raw Sequence Listing Error Summary

## ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER:

09/782,974

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 ☐ Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line.  
This may occur if your file was retrieved in a word processor after creating it.  
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2 ☐ Wrapped Aminos The amino acid number/text at the end of each line "wrapped" down to the next line.  
This may occur if your file was retrieved in a word processor after creating it.  
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3 ☐ Incorrect Line Length The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4 ☐ Misaligned Amino Acid Numbering The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5 ☐ Non-ASCII This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.  
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6 ☐ Variable Length Sequence(s) ☐ contain n's or Xaa's which represented more than one residue.  
As per the rules, each n or Xaa can only represent a single residue.  
Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.
- 7 ☐ PatentIn ver. 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) ☐. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 8 ☐ Skipped Sequences (OLD RULES) Sequence(s) ☐ missing. If intentional, please use the following format for each skipped sequence:  
(2) INFORMATION FOR SEQ ID NO:X:  
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")  
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:  
This sequence is intentionally skipped  
  
Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9 ☐ Skipped Sequences (NEW RULES) Sequence(s) ☐ missing. If intentional, please use the following format for each skipped sequence.  
<210> sequence id number  
<400> sequence id number  
000
- 10 ☐ Use of n's or Xaa's (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.  
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.  
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11 ☒ Use of <213>Organism (NEW RULES) Sequence(s) ☐ are missing this mandatory field or its response.  
  
117-119, 121, 132, 134
- 12 ☒ Use of <220>Feature (NEW RULES) Sequence(s) ☐ are missing the <220>Feature and associated headings.  
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"  
Please explain source of genetic material in <220> to <223> section.  
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13 ☐ PatentIn ver. 2.0 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other means to copy file to floppy disk.

OIPE

## RAW SEQUENCE LISTING

DATE: 03/27/2001

PATENT APPLICATION: US/09/782,974

TIME: 08:05:17

Input Set : A:\411USPHRM311.txt

Output Set: N:\CRF3\03272001\I782974.raw

Does Not Comply  
Corrected Diskette Needed

*see  
pg 6-9*

3 <110> APPLICANT: Vogeli, Gabriel  
4 Lind, Peter  
5 Wood, Linda S.  
6 Parodi, Luis A.  
8 <120> TITLE OF INVENTION: Novel G Protein Coupled Receptor  
10 <130> FILE REFERENCE: 411USPHRM311  
C--> 12 <140> CURRENT APPLICATION NUMBER: US/09/782,974  
C--> 12 <141> CURRENT FILING DATE: 2001-02-14  
12 <150> PRIOR APPLICATION NUMBER: 60/165,838  
13 <151> PRIOR FILING DATE: 1999-11-16  
15 <150> PRIOR APPLICATION NUMBER: 09/714,449  
16 <151> PRIOR FILING DATE: 2000-11-16  
18 <150> PRIOR APPLICATION NUMBER: 60/198,568  
19 <151> PRIOR FILING DATE: 2000-04-20  
21 <150> PRIOR APPLICATION NUMBER: 60/166,071  
22 <151> PRIOR FILING DATE: 1999-11-17  
24 <150> PRIOR APPLICATION NUMBER: 60/166,678  
25 <151> PRIOR FILING DATE: 1999-11-19  
27 <150> PRIOR APPLICATION NUMBER: 60/173,396  
28 <151> PRIOR FILING DATE: 1999-12-28  
30 <150> PRIOR APPLICATION NUMBER: 60/184,129  
31 <151> PRIOR FILING DATE: 2000-02-22  
33 <150> PRIOR APPLICATION NUMBER: 60/185,421  
34 <151> PRIOR FILING DATE: 2000-02-28  
36 <150> PRIOR APPLICATION NUMBER: 60/185,554  
37 <151> PRIOR FILING DATE: 2000-02-28  
39 <150> PRIOR APPLICATION NUMBER: 60/186,530  
40 <151> PRIOR FILING DATE: 2000-03-02  
42 <150> PRIOR APPLICATION NUMBER: 60/186,811  
43 <151> PRIOR FILING DATE: 2000-03-03  
45 <150> PRIOR APPLICATION NUMBER: 60/188,114  
46 <151> PRIOR FILING DATE: 2000-03-09  
48 <150> PRIOR APPLICATION NUMBER: 60/190,310  
49 <151> PRIOR FILING DATE: 2000-03-17  
51 <150> PRIOR APPLICATION NUMBER: 60/190,800  
52 <151> PRIOR FILING DATE: 2000-03-21  
54 <150> PRIOR APPLICATION NUMBER: 60/201,190  
55 <151> PRIOR FILING DATE: 2000-05-02  
57 <150> PRIOR APPLICATION NUMBER: 60/203,111  
58 <151> PRIOR FILING DATE: 2000-05-08  
60 <150> PRIOR APPLICATION NUMBER: 60/207,094  
61 <151> PRIOR FILING DATE: 2000-05-25  
63 <160> NUMBER OF SEQ ID NOS: 192  
65 <170> SOFTWARE: PatentIn version 3.0  
67 <210> SEQ ID NO: 1  
68 <211> LENGTH: 1182  
69 <212> TYPE: DNA

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/782,974

DATE: 03/27/2001

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Input Set : A:\411USPHRM311.txt

Output Set: N:\CRF3\03272001\I782974.raw

```

70 <213> ORGANISM: Homo sapiens
72 <400> SEQUENCE: 1
73 gtctgggggt ggggatgct gggacagggg tcaattgcct gaagcaagtg ctctcatccc      60
75 cctagctcct gctgatctag ttggggctcc agagtgggga ggagaaaggc actttgaaac      120
77 ttctctgccc ttaccgtctt agccatcaaa ctctgagctg gagatagtga cgatgtgaca      180
79 ggaactttcc ctgggctctt ctgggccaca attcctggcc gagagaaaga ggaggaatga      240
81 ggtgagcacc ttcttcactc ctagggccat gtggtagagc tgcagtcgca cctccttctg      300
83 ccaataggca tagatgagtg ggttgagcag ggagttgccc acgccgagca gccacaggta      360
85 ccgttccagc actaggtaga ggtgacactc ctggcaggcc acctgcacaa tgccagtgat      420
87 aaggaagggg gtccaggata gagcaaaagc cccaatgaga acagacacag tacggagagc      480
89 ttggaagtgc ctgggagtcg gtgggatcgc ataacctcca gccatggctc ctgcatgttc      540
91 catctttcga atctgctggc tgtgcatgga ggcaatcttg agcatgtcgc agtagaagaa      600
93 gacaaagagg agcatggctg ggaagaagcc aacgcaggag agggtcagca cgaagtgagg      660
95 gtgaaatata gcaaagaagc tgcaactgcc tttgtaggca gtctgctgga acatggggat      720
97 tccgagtggg aggaagccaa tgaggtaaga cactaaccac agcccggcaa tgcaggcccc      780
99 ggccacgaac ccactcatga tcttcaagta gcggaagggc tgcttgatgg caaggtaacct      840
101 gtcaaagggt atcagcatga ccgtgaggac agaggcagct gcggaggaag tgacaaatgc      900
103 catccgcagg ctgcacaggg tcttctgtgt gggccgagaa gggctggaga gctggtctgt      960
105 gagtaggcca gagatggcca caccaatcaa ggtgtcagcc acagccagat tcaagggtgaa      1020
107 gcagagactg acaccatcat tcttgtggat caacagcagc acagccacag ccactagtgt      1080
109 gttagttaga atgatgaggg aggccaggac agcaaggatc actccaaatg agaaagatga      1140
111 ttccatgtct cgaagtggca ggacttcact taccagggca tg                          1182
114 <210> SEQ ID NO: 2
115 <211> LENGTH: 335
116 <212> TYPE: PRT
117 <213> ORGANISM: Homo sapiens
119 <400> SEQUENCE: 2
121 Met Glu Ser Ser Phe Ser Phe Gly Val Ile Leu Ala Val Leu Ala Ser
122 1 5 10 15
124 Leu Ile Ile Ala Thr Asn Thr Leu Val Ala Val Ala Val Leu Leu Leu
125 20 25 30
127 Ile His Lys Asn Asp Gly Val Ser Leu Cys Phe Thr Leu Asn Leu Ala
128 35 40 45
130 Val Ala Asp Thr Leu Ile Gly Val Ala Ile Ser Gly Leu Leu Thr Asp
131 50 55 60
133 Gln Leu Ser Ser Pro Ser Arg Pro Thr Gln Lys Thr Leu Cys Ser Leu
134 65 70 75 80
136 Arg Met Ala Phe Val Thr Ser Ser Ala Ala Ala Ser Val Leu Thr Val
137 85 90 95
139 Met Leu Ile Thr Phe Asp Arg Tyr Leu Ala Ile Lys Gln Pro Phe Arg
140 100 105 110
142 Tyr Leu Lys Ile Met Ser Gly Phe Val Ala Gly Ala Cys Ile Ala Gly
143 115 120 125
145 Leu Trp Leu Val Ser Tyr Leu Ile Gly Phe Leu Pro Leu Gly Ile Pro
146 130 135 140
148 Met Phe Gln Gln Thr Ala Tyr Lys Gly Gln Cys Ser Phe Phe Ala Val
149 145 150 155 160
151 Phe His Pro His Phe Val Leu Thr Leu Ser Cys Val Gly Phe Phe Pro
152 165 170 175

```

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Input Set : A:\411USPHRM311.txt

Output Set: N:\CRF3\03272001\I782974.raw

```

154 Ala Met Leu Leu Phe Val Phe Phe Tyr Cys Asp Met Leu Lys Ile Ala
155                      180                      185                      190
157 Ser Met His Ser Gln Gln Ile Arg Lys Met Glu His Ala Gly Ala Met
158                      195                      200                      205
160 Ala Gly Gly Tyr Arg Ser Pro Arg Thr Pro Ser Asp Phe Lys Ala Leu
161                      210                      215                      220
163 Arg Thr Val Ser Val Leu Ile Gly Ser Phe Ala Leu Ser Trp Thr Pro
164 225                      230                      235                      240
166 Phe Leu Ile Thr Gly Ile Val Gln Val Ala Cys Gln Glu Cys His Leu
167                      245                      250                      255
169 Tyr Leu Val Leu Glu Arg Tyr Leu Trp Leu Leu Gly Val Gly Asn Ser
170                      260                      265                      270
172 Leu Leu Asn Pro Leu Ile Tyr Ala Tyr Trp Gln Lys Glu Val Arg Leu
173                      275                      280                      285
175 Gln Leu Tyr His Met Ala Leu Gly Val Lys Lys Val Leu Thr Ser Phe
176                      290                      295                      300
178 Leu Leu Phe Leu Ser Ala Arg Asn Cys Gly Pro Glu Arg Pro Arg Glu
179 305                      310                      315                      320
181 Ser Ser Cys His Ile Val Thr Ile Ser Ser Ser Glu Phe Asp Gly
182                      325                      330                      335
184 <210> SEQ ID NO: 3
185 <211> LENGTH: 657
186 <212> TYPE: DNA
187 <213> ORGANISM: Homo sapiens
189 <400> SEQUENCE: 3
190 cagcgcgagc gccttcacatg tgacggtgtc catgcgctgg cagtgtctgc gtgccaccgc 60
192 gtgcacctgg agcgaggtga ggcagagcac cgccagcggc agcacgaagc ccacggcatg 120
194 gagcgtggcg gtgaaggctg cgaagcgcg acgctcaggc tcgggcgggc gccgcagcga 180
196 acaggacgcg aaggcgctgc ttagccaag ccacgagcag ccaagtgcag cgcctgagaa 240
198 ggccagcgac tgtccccagg cacagcccag cagcaggccg gcatagcgcg gtcgcaggcg 300
200 tccggcgtag cgcagtgagg agcccactgc cagccactgg tctgcgtca gcgccgccac 360
202 gtcagcgccc gcgttggaag ccaggaaggt gtccaggaag ccaatgactt ggcatgcgcc 420
204 gggcgccgac ggtgtccgcc cgcgcacac accgagcagc gtgaagggca tgtccagcgc 480
206 cgccagcagc aggtggccca gagacagatt caccaggagg acgcctgagg ctcgagtgcg 540
208 gagctcagcg ctgtaggcgc aacaaagcag caccagtgcg ttggatagca gcgccacggc 600
210 cagtaccatc accaggagac ccgccagcag cgctcgcgc gggcccatgg cgctagc 657
213 <210> SEQ ID NO: 4
214 <211> LENGTH: 217
215 <212> TYPE: PRT
216 <213> ORGANISM: Homo sapiens
218 <400> SEQUENCE: 4
220 Ser Ala Met Gly Pro Gly Glu Ala Leu Leu Ala Gly Leu Leu Val Met
221 1                      5                      10                      15
223 Val Leu Ala Val Ala Leu Leu Ser Asn Ala Leu Val Leu Leu Cys Cys
224                      20                      25                      30
226 Ala Tyr Ser Ala Glu Leu Arg Thr Arg Ala Ser Gly Val Leu Leu Val
227                      35                      40                      45
229 Asn Leu Ser Leu Gly His Leu Leu Leu Ala Ala Leu Asp Met Pro Phe
230                      50                      55                      60

```

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DATE: 03/27/2001

PATENT APPLICATION: US/09/782,974

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Input Set : A:\411USPHRM311.txt

Output Set: N:\CRF3\03272001\I782974.raw

```

232 Thr Leu Leu Gly Val Met Arg Gly Arg Thr Pro Ser Ala Pro Gly Ala
233 65 70 75 80
235 Cys Gln Val Ile Gly Phe Leu Asp Thr Phe Leu Ala Ser Asn Ala Ala
236 85 90 95
238 Leu Ser Val Ala Ala Leu Ser Ala Asp Gln Trp Leu Ala Val Gly Phe
239 100 105 110
241 Pro Leu Arg Tyr Ala Gly Arg Leu Arg Pro Arg Tyr Ala Gly Leu Leu
242 115 120 125
244 Leu Gly Cys Ala Trp Gly Gln Ser Leu Ala Phe Ser Gly Ala Ala Leu
245 130 135 140
247 Gly Cys Ser Trp Leu Gly Tyr Ser Ser Ala Phe Ala Ser Cys Ser Leu
248 145 150 155 160
250 Arg Leu Pro Pro Glu Pro Glu Arg Pro Arg Phe Ala Ala Phe Thr Ala
251 165 170 175
253 Thr Leu His Ala Val Gly Phe Val Leu Pro Leu Ala Val Leu Cys Leu
254 180 185 190
256 Thr Ser Leu Gln Val His Arg Val Ala Arg Arg His Cys Gln Arg Met
257 195 200 205
259 Asp Thr Val Thr Met Lys Ala Leu Ala
260 210 215
262 <210> SEQ ID NO: 5
263 <211> LENGTH: 222
264 <212> TYPE: DNA
265 <213> ORGANISM: Homo sapiens
267 <400> SEQUENCE: 5
268 tgtgcagggtg tgatctccat tcctttgtac atccctcaca cgctgttcga atgggatttt 60
270 ggaaaggaaa tctgtgtatt ttggctcact actgactatc tgttatgtac agcatctgta 120
272 tataacattg tcctcatcag ctatgatcga tacctgtcag tctcaaatgc tgtaagtcca 180
274 acacattaat ttatccccct tagaagatta tgtaaatgta ta 222
277 <210> SEQ ID NO: 6
278 <211> LENGTH: 73
279 <212> TYPE: PRT
280 <213> ORGANISM: Homo sapiens
282 <400> SEQUENCE: 6
284 Cys Ala Gly Val Ile Ser Ile Pro Leu Tyr Ile Pro His Thr Leu Phe
285 1 5 10 15
287 Glu Trp Asp Phe Gly Lys Glu Ile Cys Val Phe Trp Leu Thr Thr Asp
288 20 25 30
290 Tyr Leu Leu Cys Thr Ala Ser Val Tyr Asn Ile Val Leu Ile Ser Tyr
291 35 40 45
293 Asp Arg Tyr Leu Ser Val Ser Asn Ala Val Ser Arg Thr His Phe Ile
294 50 55 60
296 Pro Leu Arg Arg Leu Cys Lys Cys Ile
297 65 70
299 <210> SEQ ID NO: 7
300 <211> LENGTH: 507
301 <212> TYPE: DNA
302 <213> ORGANISM: Homo sapiens
304 <400> SEQUENCE: 7

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TIME: 08:05:17

Input Set : A:\411USPHRM311.txt

Output Set: N:\CRF3\03272001\I782974.raw

```

305 gacgtcgaag caggtgatga tgcccagggc gtgcaccggg taggtgagat cgggtgcgcgc      60
307 cagcggggac agggcggtca ggagcagcag ccagggtccct gcacacgcgg ccaccgcgta      120
309 acgacggcgg cgccagcgct tggagctgag cgggtacagg atccccagga agcgctccac      180
311 gctgatacag gtcagtgtga ggatgctgga atacatgttt gcgtaaaagg ccacggtcac      240
313 cacgttgcaa agcagcaccc cgaataccca gtggtggcgg ttgcaatggt agtagatttg      300
315 gaaaggcaac acgctggcca gcatcaggtc cgtgacgctc aggttgatca tgaagatgac      360
317 cgacggggat ctggggccca tgcgcccggc cagcacccac agagagaaga ggttgcccgg      420
319 gatgctgacc gccggccacca gcgagtacac cacgggcagg gccaccgcga tcgccggggt      480
321 ccgcagcatc tgcagcgctc cgttgctc                                     507
324 <210> SEQ ID NO: 8
325 <211> LENGTH: 169
326 <212> TYPE: PRT
327 <213> ORGANISM: Homo sapiens
329 <400> SEQUENCE: 8
331 Asp Asn Ala Thr Leu Gln Met Leu Arg Asn Pro Ala Ile Ala Val Ala
332 1 5 10 15
334 Leu Pro Val Val Tyr Ser Leu Val Ala Ala Val Ser Ile Pro Gly Asn
335 20 25 30
337 Leu Phe Ser Leu Trp Val Leu Cys Arg Arg Met Gly Pro Arg Ser Pro
338 35 40 45
340 Ser Val Ile Phe Met Ile Asn Leu Ser Val Thr Asp Leu Met Leu Ala
341 50 55 60
343 Ser Val Leu Pro Phe Gln Ile Tyr Tyr His Cys Asn Arg His His Trp
344 65 70 75 80
346 Val Phe Gly Val Leu Cys Asn Leu Val Val Thr Val Ala Phe Tyr Ala
347 85 90 95
349 Asn Met Tyr Ser Ser Ile Leu Thr Met Thr Cys Ile Ser Val Glu Arg
350 100 105 110
352 Phe Leu Gly Ile Leu Tyr Pro Leu Ser Ser Lys Arg Trp Arg Arg Arg
353 115 120 125
355 Arg Tyr Ala Val Ala Ala Cys Ala Gly Thr Trp Leu Leu Leu Leu Thr
356 130 135 140
358 Ala Leu Ser Pro Leu Ala Arg Thr Asp Leu Thr Tyr Pro Val His Ala
359 145 150 155 160
361 Leu Gly Ile Ile Thr Cys Phe Asp Val
362 165
364 <210> SEQ ID NO: 9
365 <211> LENGTH: 270
366 <212> TYPE: DNA
367 <213> ORGANISM: Homo sapiens
369 <400> SEQUENCE: 9
370 cccatgttcc tgctcctggg cagcctcacg ttgtcggatc tgctggcagg cgcgcctac      60
372 gccgccaaca tcctactgtc ggggcccgtc acgctgaaac tgtccccgc gctctggttc      120
374 gcacgggagg gaggcgtctt cgtggcactc actgcgtccg tgctgagcct cctggggcatc      180
376 gcgctggagc gcagcctcac catggcgcgc agggggcccg cgcccgctctc cagtcggggg      240
378 cgcacgctgg cgatggcagc cgcggcctgg                                     270
381 <210> SEQ ID NO: 10
382 <211> LENGTH: 90
383 <212> TYPE: PRT

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09/782, 4 6

<210> 117

<211> 20

<212> DNA

<213> Artificial Sequence

*see item 12 on Error Summary sheet*

<400> 117

acagccccaagccaaacac

20

<210> 118

<211> 22

<212> DNA

<213> Artificial Sequence

*item 12*

<400> 118

ccgcaggagc aatgaaaatc ag

22

<210> 119

<211> 19

<212> DNA

<213> Artificial Sequence

*item 12*

<400> 119

ctgaaagttg tcgctgacc

19



09/782974 7

<210> 121

<211> 25

<212> DNA

<213> Artificial Sequence

item 12

<400> 121

gcataccatg aatgagccac tagac

25

09/082,974 8

<210> 132

<211> 48

<212> DNA

<213> Artificial Sequence

item 12

<400> 132

gcgtaatag actcactata gggagacctg ccacactgat gcaactcc

48

&lt;210&gt; 134

&lt;211&gt; 50

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

item 12

&lt;400&gt; 134

gcgtaatacg actcactata gggagaccgc acgccactct ttactatccc

50

FYI:

**Please Note:**

Use f n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/782,974

DATE: 03/27/2001

TIME: 08:05:18

Input Set : A:\411USPHRM311.txt

Output Set: N:\CRF3\03272001\I782974.raw

L:12 M:270 C: Current Application Number differs, Replaced Current Application No  
 L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
 L:598 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15  
 L:610 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15  
 L:637 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16  
 L:640 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16  
 L:658 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16  
 L:661 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16  
 L:971 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27  
 L:1015 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28  
 L:1018 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28  
 L:2012 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:58  
 L:4412 M:258 W: Mandatory Feature missing, <220> FEATURE:  
 L:4412 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:  
 L:4421 M:258 W: Mandatory Feature missing, <220> FEATURE:  
 L:4421 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:  
 L:4430 M:258 W: Mandatory Feature missing, <220> FEATURE:  
 L:4430 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:  
 L:4453 M:258 W: Mandatory Feature missing, <220> FEATURE:  
 L:4453 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:  
 L:4603 M:258 W: Mandatory Feature missing, <220> FEATURE:  
 L:4603 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:  
 L:4626 M:258 W: Mandatory Feature missing, <220> FEATURE:  
 L:4626 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION: